

-continued

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<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: uncultured archaeon

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<210> SEQ ID NO 21
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<210> SEQ ID NO 22
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What is claimed is:

1. A microbial composition for concurrent dechlorination of a mixture of chlorinated ethanes and chlorinated ethenes, comprising an isolated bioremediative consortium comprising strains of microorganism comprising *Clostridium*, *Acetobacter*, *Dehalobacter*, *Bacteroides*, Proteobacteria, and *Dehalococcoides*,
 wherein the bioremediative consortium is obtained by culturing microbes of a sediment sample obtained from a site contaminated with a mixture of chlorinated ethanes and chlorinated ethenes in an anaerobic medium with at least one chlorinated ethane and an electron donor selected from the group consisting of lactate, succinate, pyruvate, benzoate, propionate, and formate.
2. A microbial composition according to claim 1, wherein the consortium further comprises Methanomicrobia.
3. A microbial composition according to claim 2, wherein the consortium comprises at least one of *Methanosarcina* or *Methanosaeta*.
4. A microbial composition for concurrent dechlorination of a mixture of chlorinated ethanes and chlorinated ethenes, comprising:
 - a non-naturally occurring consortium of dechlorinatingly effective microbial species, wherein said consortium of dechlorinatingly effective microbial species comprises
 - a 16S rDNA nucleic acid sequence that has more than 99% identity to a nucleic acid sequence consisting of SEQ ID NO 1,
 - a 16S rDNA nucleic acid sequence that has more than 97% identity to a nucleic acid sequence consisting of SEQ ID NO 2, and
 - a 16S rDNA nucleic acid sequence that has more than 95% identity to a nucleic acid sequence consisting of SEQ ID NO 3.
5. A microbial composition according to claim 4, wherein the consortium further comprises at least one 16S rDNA a nucleic acid sequence that has more than 97% identity to a nucleic acid sequence consisting of SEQ ID NO 4 or SEQ ID NO 5.
6. A microbial composition according to claim 4, wherein the consortium further comprises at least one 16S rDNA a nucleic acid sequence that has more than 98% identity to a nucleic acid sequence consisting of SEQ ID NO 6.
7. A microbial composition according to claim 4, wherein the consortium further comprises at least one methyl coenzyme-M reductase nucleic acid sequence consisting of SEQ ID NO 8, SEQ ID NO 9, SEQ ID NO 10, SEQ ID NO 11, SEQ ID NO 12, SEQ ID NO 13, SEQ ID NO 14, SEQ ID NO 15, SEQ ID NO 16, SEQ ID NO 17, SEQ ID NO 18, SEQ ID NO 19, or SEQ ID NO 20.